

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Meissner, Paul S.
Coleman, Timothy A.

(ii) TITLE OF INVENTION: Human Criptin Growth Factor

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.
(B) STREET: 9410 Key West Avenue
(C) CITY: Rockville
(D) STATE: MD
(E) COUNTRY: USA
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/393,023
(B) FILING DATE: 09-SEP-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/471,371
(B) FILING DATE: 06-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marks, Michelle S.
(B) REGISTRATION NUMBER: 41,971
(C) REFERENCE/DOCKET NUMBER: PF200D1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 301-309-8504
(B) TELEFAX: 301-309-8439

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA	48
Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala	
1 5 10 15	
TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC	96
Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn	
20 25 30	
GGC GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG	144
Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln	
35 40 45	
TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC	192
Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser	
50 55 60	
GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CGG GCT TTC	240
Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe	
65 70 75 80	
GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC	288
Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr	
85 90 95	
TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC	336
Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg	
100 105 110	
TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC	384
Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His	
115 120 125	
GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG	432
Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly	
130 135 140	
GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA	480
Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys	
145 150 155 160	
GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC	528
Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro	
165 170 175	
AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC	576
Ser Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg	
180 185 190	
CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG	624
Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln	
195 200 205	
CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA	672
Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu *	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
1 5 10 15

Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
20 25 30

Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
35 40 45

Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
50 55 60

Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
65 70 75 80

Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
85 90 95

Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
100 105 110

Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
115 120 125

Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
130 135 140

Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
145 150 155 160

Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Ala Pro
165 170 175

Ser Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg
180 185 190

Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln
195 200 205

Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu *
210 215 220

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTCTTGGAT CCAATTGGG AAACAGCTAT CAAAGA

36

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC

42

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT

36

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	His	Ala	Ala	Ile	Ser	Lys	Val	Phe	Glu	Leu	Gly	Leu	Val	Ala	Gly
1															
															15
Leu	Gly	His	Gln	Glu	Phe	Ala	Arg	Pro	Ser	Arg	Gly	Tyr	Leu	Ala	Phe
															30
Arg	Asp	Asp	Ser	Ile	Trp	Pro	Gln	Glu	Glu	Pro	Ala	Ile	Arg	Pro	Arg
															45
Ser	Ser	Gln	Arg	Val	Pro	Pro	Met	Gly	Ile	Gln	His	Ser	Lys	Glu	Leu
															50
															55
															60
Asn	Arg	Thr	Cys	Cys	Leu	Asn	Gly	Gly	Thr	Cys	Met	Leu	Gly	Ser	Phe
															65
															70
															75
															80
Cys	Ala	Cys	Pro	Pro	Ser	Phe	Tyr	Gly	Arg	Asn	Cys	Glu	His	Asp	Val
															85
															90
															95
Arg	Lys	Glu	Asn	Cys	Gly	Ser	Val	Pro	His	Asp	Thr	Trp	Leu	Pro	Lys
															100
															105
															110
Lys	Cys	Ser	Leu	Cys	Lys	Cys	Trp	His	Gly	Gln	Leu	Arg	Cys	Phe	Pro
															115
															120
															125
Gln	Ala	Phe	Leu	Pro	Gly	Cys	Asp	Gly	Leu	Val	Met	Asp	Glu	His	Leu
															130
															135
															140
Val	Ala	Ser	Arg	Thr	Pro	Glu	Leu	Pro	Pro	Ser	Ala	Arg	Thr	Thr	Thr
															145
															150
															155
															160
Phe	Leu	Met	Val	Gly	Ile	Cys	Leu	Ser	Ile	Gln	Ser	Tyr	Tyr		
															165
															170